

Sequence Listing

SEQ ID NO:1

Sequence (accession NO: APE1094 of Aeropyrum pernix K1)

gtgggggtgtc tggtttttggc ttctagctct ggggggtgttg gaggcggtga catgcctttc 60
aagcccgtgg ctgaggcctt cgcctccatg gagaggataa cctctaggac gcagctcacc 120
ctcctcctca caaggctctt caagtccacg cccccggggg cgatcggtat tgtggtgtac 180
ctgatccagg ggaagctggg gcccgactgg aaggggctgc cggagctggg tgcggggag 240
aagctgcttg taaaggccat agccctggct tacaaggcca ctgaggagag ggttgagagg 300
ctctacaagt ctgtaggcga cctggggagt gtggccgaga ggctgtcgcg ggagtaccgc 360
tcccgggctg ccagggccgt caccctggag gcgttcattg cgggaggggg ggaggcgctg 420
actgtgagga gggttttacaa cacgctgtac aggatagcca tggcgagggg tgaggggagc 480
agggacatca agcttaggct gctggccggc ctctggcgcg acgccgagcc cgtggaggcg 540
aagtatatgt tgagggtttgt ggaggggagg ctgaggggtg gtgttgggga cgcgaccgtc 600
ctcgacgcc tcgccaatggc cttcggcggc ggggcccacg cgaggcccgt tatagagagg 660
gcctacaacc tcagggccga cctaggctac atagcggagg tcgtggccag ggaggggtgtt 720
gatgcgctga ggggtgtgaa gccccaggct gccgttccta taaggccgat gctggccgag 780
agggggaggg acccggtga gatactcagg aaggtggggg gcagggtgt cgtcgagtat 840
aagtacgatg gggagagggc gcagatacac aagaaggacg gggaggtcta catctactcg 900
aggaggcttg agaacataac caggatgttc cccgacgtgg ttgagatggc gaggaagggc 960
ctcaaagccg gggaggctat agtcgagggg gagatagtgg ccgtagacct agacaactat 1020
gagatacagc ccttccaggt cctcatgcag aggaagagga agcacgacat acacagggtc 1080
atgagggagg tgcccgtcgc cgtcttcctc ttcgacgcc tctacgtgga cggcgaggac 1140
ctcacaagca aaccctccc cgagaggcgc aggaggctca aggagatagt tgtggagacg 1200

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cccctctgga ggctggcgga gtccatcgag accagcgacc ccgaggagct gtggaccttc 1260
 ttctgaagg ccatagagga gggggccgag ggcgtcatgg tcaaggccgt ccacagggaac 1320
 tcagtctaca ccgcgggcgt aaggggggtg ctgtgggtca agctgaagag ggattacaag 1380
 agcgagatga tggacacggt ggacctcgta gtgggtggcg ccttctacgg cagggggaag 1440
 aggggcggga agctcagcag cctgctcatg gccgcctacg accagacag ggacgtgttc 1500
 cccaccgtct gcaagggtggc cacagggttc acggacgagg agctggacag gatgaacgag 1560
 atgctgaaga agcacatcat accaggaag caccgaggg tagagtcgag gatagagcct 1620
 gacgtgtggg tggagcccg cctcgtggcg gagatactgg gcgccgagct caccctctca 1680
 ccaatgcaca cctgctgcct caacactgtg aggccggggg tggggataag cataagggttc 1740
 cccaggttca taagggtggag ggacgacaag agtccggagg acgcgacaac aaccacgag 1800
 ctgctcgaga tgtacaagag gcagttgagg aggggtgaag agccggcgga gcaggtgtag 1860

SEQ ID NO:2

Amino acid sequence (accession NO: APE1094 of *Aeropyrum pernix* K1)

Val Gly Cys Leu Val Leu Ala Ser Ser Ser Gly Gly Val Gly Gly Gly
 1 5 10 15
 Asp Met Pro Phe Lys Pro Val Ala Glu Ala Phe Ala Ser Met Glu Arg
 20 25 30
 Ile Thr Ser Arg Thr Gln Leu Thr Leu Leu Leu Thr Arg Leu Phe Lys
 35 40 45
 Ser Thr Pro Pro Gly Ala Ile Gly Ile Val Val Tyr Leu Ile Gln Gly
 50 55 60
 Lys Leu Gly Pro Asp Trp Lys Gly Leu Pro Glu Leu Gly Val Gly Glu

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65	70	75	80
Lys Leu Leu Val	Lys Ala Ile Ala Leu Ala	Tyr Lys Ala Thr	Glu Glu
85	90	95	
Arg Val Glu Arg	Leu Tyr Lys Ser Val Gly Asp	Leu Gly Ser Val	Ala
100	105	110	
Glu Arg Leu Ser	Arg Glu Tyr Arg Ser Arg Ala Ala	Arg Ala Val Thr	
115	120	125	
Leu Glu Ala Phe	Met Ala Gly Gly Gly Glu Ala Leu Thr	Val Arg Arg	
130	135	140	
Val Tyr Asn Thr	Leu Tyr Arg Ile Ala Met Ala Gln	Gly Glu Gly Ser	
145	150	155	160
Arg Asp Ile Lys	Leu Arg Leu Leu Ala Gly Leu Leu Ala	Asp Ala Glu	
165	170	175	
Pro Val Glu Ala	Lys Tyr Ile Val Arg Phe Val Glu Gly	Arg Leu Arg	
180	185	190	
Val Gly Val Gly	Asp Ala Thr Val Leu Asp Ala Leu Ala	Met Ala Phe	
195	200	205	
Gly Gly Gly Ala	His Ala Arg Pro Val Ile Glu Arg Ala Tyr	Asn Leu	
210	215	220	
Arg Ala Asp Leu	Gly Tyr Ile Ala Glu Val Val Ala Arg	Glu Gly Val	
225	230	235	240
Asp Ala Leu Arg	Gly Val Lys Pro Gln Val Gly Val Pro Ile	Arg Pro	
245	250	255	
Met Leu Ala Glu	Arg Gly Arg Asp Pro Ala Glu Ile Leu Arg	Lys Val	
260	265	270	

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Gly Gly Arg Ala Val Val Glu Tyr Lys Tyr Asp Gly Glu Arg Ala Gln			
275	280	285	
Ile His Lys Lys Asp Gly Glu Val Tyr Ile Tyr Ser Arg Arg Leu Glu			
290	295	300	
Asn Ile Thr Arg Met Phe Pro Asp Val Val Glu Met Ala Arg Lys Gly			
305	310	315	320
Leu Lys Ala Gly Glu Ala Ile Val Glu Gly Glu Ile Val Ala Val Asp			
	325	330	335
Pro Asp Asn Tyr Glu Ile Gln Pro Phe Gln Val Leu Met Gln Arg Lys			
340	345	350	
Arg Lys His Asp Ile His Arg Val Met Arg Glu Val Pro Val Ala Val			
355	360	365	
Phe Leu Phe Asp Ala Leu Tyr Val Asp Gly Glu Asp Leu Thr Ser Lys			
370	375	380	
Pro Leu Pro Glu Arg Arg Arg Arg Leu Lys Glu Ile Val Val Glu Thr			
385	390	395	400
Pro Leu Trp Arg Leu Ala Glu Ser Ile Glu Thr Ser Asp Pro Glu Glu			
	405	410	415
Leu Trp Thr Phe Phe Leu Lys Ala Ile Glu Glu Gly Ala Glu Gly Val			
420	425	430	
Met Val Lys Ala Val His Arg Asp Ser Val Tyr Thr Ala Gly Val Arg			
435	440	445	
Gly Trp Leu Trp Val Lys Leu Lys Arg Asp Tyr Lys Ser Glu Met Met			
450	455	460	
Asp Thr Val Asp Leu Val Val Val Gly Ala Phe Tyr Gly Arg Gly Lys			

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465	470	475	480
Arg Gly Gly Lys Leu Ser Ser Leu Leu Met Ala Ala Tyr Asp Pro Asp			
	485	490	495
Arg Asp Val Phe Pro Thr Val Cys Lys Val Ala Thr Gly Phe Thr Asp			
	500	505	510
Glu Glu Leu Asp Arg Met Asn Glu Met Leu Lys Lys His Ile Ile Pro			
	515	520	525
Arg Lys His Pro Arg Val Glu Ser Arg Ile Glu Pro Asp Val Trp Val			
	530	535	540
Glu Pro Ala Leu Val Ala Glu Ile Leu Gly Ala Glu Leu Thr Leu Ser			
	545	550	555
Pro Met His Thr Cys Cys Leu Asn Thr Val Arg Pro Gly Val Gly Ile			
	565	570	575
Ser Ile Arg Phe Pro Arg Phe Ile Arg Trp Arg Asp Asp Lys Ser Pro			
	580	585	590
Glu Asp Ala Thr Thr Thr His Glu Leu Leu Glu Met Tyr Lys Arg Gln			
	595	600	605
Leu Arg Arg Val Glu Glu Pro Ala Glu Gln Val			
	610	615	

SEQ ID NO:3

GGCTGTCTGGTTTTGGCTTCT

SEQ ID NO:4

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GTGAAGGGATCCTTACACCTGCTCCGC

SEQ ID NO:5

TAAGCTCCGGATTGTCCGGGAGGTAAAGCCCTGAT

SEQ ID NO:6

CACAGGAAGCTCTACAGGTACTCCG

SEQ ID NO:7

TGGTCATCAGGGCTTTACCTCCCGGACATTCCGGACCTTACGGAGTACCTGTAGAGCTTCCTGTGCAAGC